FILE 'USPAT' ENTERED AT 16:23:34 ON 13 MAY

\* THE WEEKLY PATENT TEXT AND IMAGE DATA IS CUFRENT \*

\* THROUGH May 11, 1999.

-+

=> s estrogen?(5a)receptor?

4724 ESTROGEN? 38183 FECELTOR?

L1 934 ESTECGEN? (5A) FECEPTOR?

=> s 11 and shimer:

5349 CHIMEE? LL 131 LT AML CHIMER:

=> s 12 and orphan?

B 77 ORPHAN? L3 04 L1 ANI ORPHANI

=> d 1-24

- 1. 5,891,700, Apr. ., 1999, Feceptor-type phosphotyrosine phosphatase-.gamma.; Joseph Schlessinger, 435/196 [IMAGE AVAILABLE]
- 2. 5,877,207, Mar. \_, 1999, Synthesis and use of retincid compounds having negative horm ne and/or antagonist activities; Elliott S. Klein, et al., 514,456; 549 405 [IMAGE AVAILABLE]
- 3. 5,876,951, Mar. \_, 1999, Yeast cells engineered to produce pheromone system protein surrorates and uses therefor; Dana M. Fowlkes, et al., 435/7.31, 254.11, 254.2, 254.21 [IMAGE AVAILABLE]
- 4. 5,374,5-4, Fer. 23, 1999, Mutated steroid hormone redeptors, methods for their use and nolecular switch for gene therapy; Elisabetta Vegeto, et al., 530-350; 536,23.1, 24.1 [IMAGE AVAILABLE]
- 5. 5,849,435, Iec. 15, 1998, Liver enriched transcription factor; Frances M. Sladek, et al., 435/6; 536/24.1 [IMAGE AVAILABLE]
- 6. 5,834,213, Nov. 10, 1998, Screening system and assay for identifying compounds that regulate steroid and **orphan** receptors mediation of DNA

transcription; Bert W. O'Malley, et al., 435/7.8, 6, 7.2, 6).1, 320.1; 520.23.1 IMAGE AVAILABLE

- 7. 5,789,184, Aug. 4, 1938, Yeast cells enumeered to produce pheromone system protein sirrogates, and uses therefor; Dana M. Fowlkes, et al., 475(7.31, 254.11, 254.2, 254.21 [IMAGE AMAILABLE]
- 8. 5,780,361, Jul. 28, 1993, Method of treating Hormone independent cancer; Arnor Frongrad, 514(28) [IMAGE AVAILABLE]
- 9. 5,776,639, Jul. 7, 1998, Method of identifying negative hormone and/or antagenist activities; Elliott S. Klein, et al., 435/7.2, 7.1, 63.1, 326.1, 325 [MAGE AVAILABLE]
- 18. 5,756,448, May 26, 1998, Constitute activator of retinoid (CAR) receptor polypertides; Lavid D. Moore, et al., 514/2; 435/68.1; 520/350 [IMAGE AVAIJABLE]
- 11. \*,710,017, Jan. 20, 1998, DNA encoding a constitutive activator retinuic acti response (CAF) receptor; David I. Moore, et al., 435/69.1, 31-.1, 328; 528/20.8 IMAGE AVAILABLE
- 11. 5,710,004, Jan. 20, 1998, Methods of using novel steroid himbne orphan redeptors; Fonsid M. Evans, et al., 435/0, 6:1, 69.4, 69.7, 3.0.1, 3.05; 590/350; 535/20.1 [IMAGE EVALLABIE]
- 17. 8,737,800, Jan. 13, 1008, Retinoic acid response elements and assays employing same; David John Mangelsdorf, et al., 43576, 7.2, 7.21, 7.8, 80.1, 310.1, 325, 349, 358, 367; 536/23.1, 23.2 [IMAGE AVAILABLE]
- 14. 5,096,033, Dec. 9, 1997, Orphan steroid hirmine receptors; Einald M. Ewans, et al., 539/350, 358 [IMAGE AVAILABLE]
- is. 5,686,974, Nov. 11, 1997, Constitutive attraction of retinoid acid cusp nse (car. receptor fusion protien; David E. M.ore, et al., 680/250; 4.5/69.1, 69.3; 836/12.4 [IMAGE AVAILABLE]
- 17. 5,679,118, Oct. 11, 1997, Method for finding transcription. activating of the NEE steroid hormone 1-ceptor; Estan Friedman, et al., 4/5/6, 7.1 [IMAGE AVAILABLE]
- 17. 5,639,616, Jun. 17, 1997, Isolated nucleic acid encoding a uniquitous nuclear receptor; Shutsung Liac, et al., 435/7.1, 69.1, 252.3, 320.1; 536/22.5, 24.3 [IMAGE AVAILABLE]
- 18. 5,607,967, Mar. 4, 1997, Treatment of alzheimer's disease with

of hRXR-alpha; or %=(\*etraderyl:xy)=2=furan carboxylic acid; B. (i) about 55\* amino acid sequence Eitan Friedman, et al., 814/461, 473 [IMAGE AVAILABLE] identity with the DNA binding domain of hRAE-alpha; (ii) about 56% amino acid sequence identity 19. 5,604,115, Feb. 18, 1997, Liver enriched with the DNA binding domain .ranscription factor; of hTF-peta; Frances M. Sladek, et al., 435/69.1, 252.3, (iii) about 50\* amino acid sequence identity 54.11, 330.1, 325, 348; with the CNA binding domain 1367\_3.5 [IMAGE ATAILABLE] of hGE; and (iv) about 72% amino acid sequence identity 20. 5,602,009, Feb. 11, 1997, Dominant with the SNA binding domain negative chimeras of the of hRXF-airna; or steroid/thyroid superfamily of receptors; C. (i) at 1 5/8 amino acid sequence identity w.t. the DNA binding K hald M. Evans, ot al., 485/69.7, 252.3, 320.1; 530/350; 536/23.4 [IMAGE AVAILABLE] domain :: ::RAW-alpha; (ii) about %:\* amino acid sequence identity with the INA bunding domain 21. 5,537,693, Jan. 28, 1997, Hormone of hT9-k-ti: response element compositions and assay; Ronald M. Evans, et al., 435/6, 69.7; (iii) alc :t 40\* amino acid sequence identity with the DMA binding domain 530/330, 350 'IMAGE of hGF; :n1 (iv) at 9: 62) amino acid sequence identity with the EMA binding domain AVAILABLEL 21. 5,556,956, Sep. 17, 1996, Methods and of hRMA-alpha; or D. (i)  $\pm \epsilon$  it 5.3% amino acid sequence identity with the DNA binding rempositions relating to the androgen recepto: jene and uses thereof; Arun F. Roy, et al., 135/24.1, domain :: ::FAR-alpha; 23.1, 24.3, 24.31 (IMAGE AVAILABLE) (ii) about 52% amino acid sequence identity with the INA kinding domain \_s. 5,530,123, 'ul. 2, 1996, Receptor-type of hTS-teta; (iii) ap: 15 44% amino acid sequence identity ph sphotyrosine phosphatase-.gamma.; Joseph Schlessinger, with the CUA linding domain 435/6, (9.1, 69.\*, 70.1, 71.2, 195, 251.3, 254., 320.1, 357, 365; 536/23.1, of hGF; und (iv) at 1.1 61% amino acid sequence identity 23.2 [IMAGE AVAILABLE] with the LNA binding domain of hRXE-sipha; or 24. 5,364,791, Mcv. 15, 1994, Progesterone E. (i) ak: 1 59% amino acid sequence receptor having t. terminal identity with the DNA binding domain of nRAE-alpha; horsone binding tomain truncations; Elisapetta Vegéto, et al., 435/320.1, (ii) alc.t. 55% amino acid sequence identity .8; 530/350; 535/23.1 [IMAGE AVAILABLE] with the INA tinding domain of hT5-reta; (iii) ab ut 10% amino acid sequence identity = . d 14 clms with the TNA rending domain of hGh; and 9,696,233 [IMAGE AVAILABLE] (iv) about 65% amino acid sequence identity UF PAT NO: with the DNA binding domain ]: 14 of 24 of hRMF-alpha. CLAIMS: CLMS(2. CLMS [1] 2. A polypertide according to claim 1 wherein the IMA binding domain of That which is claimed is: said p:l;p=ptrde has: 1. A polypeptize characterized by having a (i) action 68% amino acid sequence identity INA binding domain comprising with the MMA kinding domain acout 66 amino acids with 9 Cys residues, of hFAF-alpha; (ii) at u. 59% amino acid sequence identity wherein said DNA binding demain is further characterized by the following with the DMA kinding domain amino acid sequence identity, of hTF-beta; relative to the DNA binding domains of hRARsipha, hTR-beta, hGR and

(iii) arout 45% amino acid sequence identity with the DNA rinding domain of hist and

(iv) ab ut 6% amino acid sequence identity with the ENA cinding domain of NAXE-alpha.

CLMS (3)

PRXR-alpha, respectively:

domain of hRAR-alpha;

if hTR-beta;

of hGR; and

identity with the DNA binding

with the DNA binding domain

with the DNA binding domain

with the DNA binding domain

A. (i) about 63% amino acid sequence

(ii) about 59% amino acid sequence identity

(iii) about 45% amino acid sequence identity

(iv) about 65\* amino acid sequence identity

3. A pclypeptide according to claim 2 wherein the ligand binding domain of said polypeptide has: (i) about 27% amino acid sequence identity with the ligand binding

(ii) about 58% amine acid sequence identity i main f nRAR-alpha; with the DNA binding domain illy about 30% amin: arid sequence identity of hTk=beta; (iii) aktur 48% amin. avid sequence identity with the ligand binding. d main of hTR-beta; with the DNA binding d main (iii) about 30% amin. abid sequence identity of hGR; and with the ligand binding (iv) about 60% amino acid sequence identity dimain of hGR; and with the DNA binding domain (17) about 22% amino acid sequence identity of hRXR-alpha. with the ligand binding i main | f hRXR-alpha. CLMS(9) 9. A polypeptide according to claim & wherein the ligand binding domain 4. A polypeptide according to claim 3 of said polypeptide has: wherein said polypeptide has an (1) about 19% amino acid sequence identity .ve:all amine acid sequence identity of: with the ligand binding (i) about 32% relative to hRAR-alpha; domain of hRAF-alpha; (ii) about 31% relative to hTR-beta; (ii) about 27% amino acid sequence identity (iii) about 18% relative to hGR; and with the ligand binding (iv) about 29% relative to hRXR-alpha. domain of hTF-beta; (iii) about 21% amino acid sequence identity with the ligand binding CLMS(5) domain of hGR; and 5. A polypeptide according to claim 1 (iv) about 25% amino acid sequence identity wherein the DNA binding domain of with the ligand binding said polypeptide has: domain of hFXR-alpha. (i) about 55% amino acid sequence identity with the DNA binding domain CIMS(10) .f hRAR-alpha; (ii) about 56% amino acid sequence identity 10. A polypertide according to claim 9 with the DNA bunding domain wherein said polypeptide has an overall amino acid sequence identity of: of hTk-beta: (iii) about 50% amino acid sequence identity :i) about 32% relative to hRAR-alpha; (ii) about 31% relative to hTR-beta; with the DNA binding demain (iii) about 25% relative to hGR; and of hGF.; and (iv) about 52% amino acid sequence identity (iv) about 33% relative to hRXR-alpha. with the DNA binding domain of hRMR-alpha. CLMS(11) 11. A polypertide according to claim 1 CLMS(6) wherein the DNA binding domain of 6. A polypeptide according to claim 5 said polypeptide has: wherein the ligand binding domain (i) about 59% amino acid sequence identity of said polypeptide has: with the DNA binding domain (i) about 32% amino acid sequence identity of hRAR-alpha; with the ligand binding (ii) about 523 amino acid sequence identity domain of hRAR-alpha; with the DNA binding domain (ii) about 29% amino acid sequence identity of hTR-beta; (iii) about 14% amino acid sequence identity with the ligand binding domain of hTR-beta; with the ENA binding domain (iii) about 20% amino acid sequence identity of hGF.; and (iv) about 61% amino acid sequence identity with the ligand binding with the DNA cinding domain d.main of hGR; and (iv) about 23% amino acid sequence identity of hRXR-alpha. with the ligand binding domain of nRXR-alpha. CLMS(12 12. A polypertide according to claim 11 CLMS (7) wherein the ligand binding 7. A polypeptide according to claim 6 domain of said polypeptide has: wherein said polypeptide has an (i) about 194 amino acid sequence identity veral, amino acid sequence identity of: with the ligar.d binding (i) about 33% relative to hRAR-alpha; domain of h.A.R-alpha; (ii) about 31% relative to hTR-beta; ii) about 2.% amino acid sequence identity (iii) about 24% relative to hGR; and with the ligand binding (iv) about 27% relative to hRXR-alpha. domair of LTE-beta; (iii) about 20% amino acid sequence identity with the ligand binding domair of hGR; and (iv) about 27% amino acid sequence identity 4. A polypeptide according to claim 1 wherein the DNA binding domain of with the ligand binding said polypeptide has: domain of hRXR-alpha. :i) about 62% amino acid sequence identity with the DNA binding demain CLMS(13)

t ERAR-alpha;

demain of hFXR-alpha; or B. (i) about 32% amino acid sequer to 16. A polypoptide absorbing to claim 12 identity with the ligand binding viberein sail polypeptide has an terall amin and sequence identity of: 1, about 17% relative to hRAR-alpha; domain of hFAR-alpha; (ii) about 29. amino acid sequence identity ii: about 24% relative to hTR-beta; (iii) about 20% relative to hGR; and with the ligan; binding domain of hTF-beta; (iii) about 2 % amino acid sequence identity (iv) about 29% relative to hRXR-alpha. with the ligar, binding domain of hGF; and (iv) about 23. amino acid sequence identity with the ligan: binding 14. A priykeptide according to claim 1 domain of hEER-alpha; or wherein the DNA binding domain of C. (i) about . A amino acid sequence identity with the ligand binding Jain p lypeptide has: (i) about 50% amino acid sequence identity domain of hFAR-alpha; with the DNA binding domain (ii) accort N \* amin: avid sequence identify f hRAR-aipha; with the ligan: binding (ii) about 55% amino abid sequence identity domain of hTrt-beta; with the DNA binding domain (iii) about : 1\* amino acid sequence identity if hTR-beta; with the ligan: binding (iii) about 50% amino acid sequence identity domain of hGF; and with the DNA binding domain (iv) about 2.4 amino acid sequence identity f hGR: and with the ligan: binding (iv) about 65% amino acid sequence identity domain of hEEF-alpha; or with the DNA binding domain D. i) about : \*\* amino acid sequence identity of hRXR-alpha. with the ligan: binding domain of hist-alpha; :LMS(15) (ii) about 2. \* amino acid sequence identity with the ligan: binding 15. A polypeptide according to claim 14 domain of hTF-peta; Therein the ligand binding (iii) about . : amino acid sequence identity immain of said polypeptide has: (i) about 18% amino acid sequence identity with the ligand binding domain of hik; and with the ligand binding (iv) about 2 \* amino acid sequence identity domair of hRAR-alpha; with the ligant binding (ii) about 20% amino acid sequence identity domain of hamm-alpha; or with the ligand binding E. (i) about 18% amino adid sequence irmain of hTk-peta; identity with 'me ligand binding (iii) about 20% amino acid sequence identity domain of haas-alpha; with the ligand binding (ii) about 2 \* amine acid sequence identity domain of hGR; and with the ligan ! binding (iv) about 24% amino acid sequence identity domain of hTF-beta; with the ligand binding (iii). about .  $\ensuremath{\%}$  amino acid sequence identity with the ligand binding domain of hRXR-alpha. domain of h :; and :LMS(16) (iv) about 24\* amino acid sequence identity 16. A polypeptide according to claim 15 with the ligand binding domain of hFEE-alpha. wherein said polypeptide has an verall amino acid sequence identity of: CLMS(18) /i) about 24% relative to hRAR-alpha; (ii) about 28% relative to hTR-beta; 18. A polyperide according to claim 1 (iii) about 13% relative to hGR; and wherein said colypeptide has an (iv) about 33% relative to hRXR-alpha. overall amino acid sequence identity, relative to hakk-alpha, hTR-bea, :LMS(17) hGF and hRXR-slpha, respectively of: A. (i: about '2% relative to hFAR-alpha; 17. A polypeptide according to claim 1(i:) about 3:\* relative to hTR-beta; wherein the ligand binding domain (iii) about 14% relative to hGF; and of said polypeptide is further characterized (i'') about 2 if relative to hRXF-alpha; or my the following amino acid B. (i. about 13% relative to hFAR-alpha; sequence identity, relative to the ligand (ii) about 31: relative to hTR-beta; : inding demains of hRAR-alpha, (iii) about .4% relative to hGE; and TR-beta, hGR and hRXR-alpha, respectively: (iv) about 2 relative to hRXR-alpha; or C. (i) about firelative to hRAR-alpha. A (i) about 27% amino acid sequence identity with the ligand binding (ii) about 319 relative to hTR-beta; domain of hRAR-alpha; (i.i) about Lik relative to hGF; and (ii) about 30% amino acid sequence identity (i) about 34 relative to hRXF-alpha; if with the ligand binding D. (i) about .7% relative to hEAR-alpha; drmain of hTR-beta; (ii) about 24. relative to hTR-beta; (iii) about 20amino acid sequence identity

with the ligand binding

with the ligand binding

(iv) about 22% amino acid sequence identity

dimain of hGR; and

(iii) about 1 % relative to hGE; and

(ii) about Lot relative to hTR-beta;

(iv) about : "elative to hRXR-alpha; r

E. (i) about .4% relative to hEAR-alpha;

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ill as it less relative to musk; and
 ive about sociative to hRXR-alpha.
19. A polymeptide apporting to planm 1
wherein said polypeptide has the
same amin- acid sequence as polypeptides
Delegged from SEQ ID NOS:2, 4,
6, 8, 10, 12 or 14.
HIMS(L0)
 ... A chimeric receptor comprising an amino-
·erminal domain, a
ENA-kinding domain, and a ligand-binding
armair,
 wherein at least one of the domains thereof
 is derived from the
  polypeptide of claim 1; and
 wherein at least one of the domains thereof
 is delized from at least one
  _{\mbox{\scriptsize previously}} identified member of the
 Precidentricid superfamily of
  :epeptors.
 <sub>2> 3</sub> 5696233/pm
             1 5696233/PN
 => s 11 and 14
             1 L1 AND L4
 => d kwic
                5,696,233 [IMAGE AVAILABLE]
 US FAT NO:
  <u>15: 1 of 1</u>
  SUMMAR(:
  BSUM(6)
   A number of receptor proteins, each specific
  for one of several classes
  of cognate steroid hormones [e.g., estrogens
  estrogen
  receptor), progesterones (progesterone
  receptor), glucocorticoid
  . allocarticald receptor), androgens
   (androgen receptor), aldosterones
   (mineralocorticoid receptor), vitamin D
   (vitamin D receptor)), retincids
   (e.g., retinoic acid receptor) or. . .
   SUMMARY:
   PSUM(11)
        . . growth hormone genes, responsive
   to glucocorticoids,
   estrogens and thyroid hormones; the
   transcriptional control units for
   mammalian prolactin genes and progesterone
   receptor jenes, responsive
   estrogens; the transcriptional control
    units for avian ovalbumin
   genes, responsive to progesterones; mammalian
   metallothionein gene
   transcriptional control units, responsive to
    glucecorticoids;. . .
    DETDESC:
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DETD(66)
wherein . . . least the previously identified member of the
       steroid/thyroid superfamily of recept is
  e.g., glucocorticoid reception (GR), thyroid reception (TR), retining the control of the control
  receptors (RAR),
        mineralocorticoid receptor (Mk), estrogen
  receptor (ER),
        the estrogen related receptors (e.g., hERR]
   or hERR2), retincid
X receptors (e.g., RXK.alpha., RXK.keta. :
    RXR.delta.), vitamin D
        receptor (VDR), aldosterone receptor (AR),
     progesterone. . .
     => d his
                             (FILE 'USPAT' ENTERED AT 16:23:34 ON 13
    MAY 1999)
                                                             934 S ESTROGEN? (5A) RECEPTOR:
     L1
                                                            181 S L1 AND CHIMER?
      L2
                                                                24 S L2 AND ORPHAN?
      1.3
                                                                   1 S 5696233/PN
     1.4
                                                                      1 S L1 AND L4
      L5
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